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Score of self comparison: 103.997

1 [DNA amplification method tolerant to sample degradation.](#) Score: 94.2
 G Wang, E Maher, C Brennan, L Chin, C Leo, M Kaur, P Zhu, M Rook, Jl. Wolfe, GM Makrigiorgos. *Genome research*, 2004, Nov., 14(11): 2357-66. PMID: 15520297 Ratio:0.91

2 [Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation.](#) Score: 92.15
 MD Robinson, C Stitzaker, AL Statham, MW Coolen, JZ Song, SS Nair, D Strelac, TP Speed, SJ Clark. *Genome research*, 2010, Dec., 20(12): 1719-29. PMID: 21045081 Ratio:0.89

3 [Cervical metastasis: diverse genome-wide DNA methylation profiles.](#) Score: 78.55
 GE Ananiew, S Goldstein, R Runneheim, DK Forrest, S Zhou, K Potamitis, CP Churas, V Bergendahl, JA Thomson, DC Schwartz. *BMC molecular biology*, 2008, , 9(1):68. PMID: 18667073 Ratio:0.76

4 [Isothermal whole genome amplification from single and small numbers of cells: a new era for preimplantation genetic diagnosis of inherited disease.](#) Score: 73.55
 AH Handyside, MD Robinson, RJ Simpson, MB Omar, MA Shaw, JG Grudzinskas, A Rutherford. *Molecular human reproduction*, 2004, Oct., 10 (10): 767-72. PMID: 15322244 Ratio:0.71

5 [Whole genome amplification--opportunities and challenges.](#) Score: 71.96
 TL Hawkins, JC Detter, PM Richardson. *Current opinion in biotechnology*, 2002, Feb., 13(1): 65-7. PMID: 11849960 Ratio:0.69

6 [Specific and complete human genome amplification with improved yield achieved by phi29 DNA polymerase and a nested primer strategy.](#) Score: 68.26
 O Almadi, F Alkayal, D Monies, BF Meyer. *BMC research notes*, 2009, , 2(1): 48. PMID: 19309528 Ratio:0.66

7 [High-throughput of whole genome amplified mouse esophageal DNA.](#) Score: 64.94
 KM Gillespie, SJ Valowin, JI Sambuhi, KM Hunter, DA Savage, D Middleton, JA Todd, PJ Bingley, EA Gale. *Tissue antigens*, 2000, Dec., 56(6): 530-8. PMID: 11169243 Ratio:0.62

8 [Quantitative analysis of DNA methylation after whole genome amplification of a minute amount of DNA from body fluids.](#) Score: 60.62
 T Vaissière, C Cuénin, A Paliwal, P Vinesi, G Hoek, M Krzynowski, I Airoldi, A Dunning, S Garte, P Hainaut, C Malavelle, K Overvad, F Clavel-Chapelon, J Linseisen, H Boeing, A Trichopoulou, A Katsalidi, D Palli, V Krogh, R Tumino, S Panico, HB Bueno-De-Mesquita, PH Peeters, M Kunkle, CA Gonzalez, C Martinez, M Dorronso, A Barricarte, C Navarro, JR Quirós, G Berglund, L Janzon, B Jarhult, NE Day, TJ Key, R Saracci, R Kaaks, E Riboli, P Hainaut, Z Hercog. *Epigenetics : official journal of the DNA Methylation Society*, 2009, May., 4(4): 221-30. PMID: 19458486 Ratio:0.58

9 [Assessment of whole genome amplification-converted bias, linear or high throughput, may give variable whole genome sequencing.](#) Score: 60.58
 R Pinard, A de Winter, GJ Sarkis, MB Gerstein, KR Tartaro, RN Plant, M Egholm, JM Rothberg, JH Leamon. *BMC genomics*, 2006, , 7(1): 216. PMID: 16928277 Ratio:0.58

10 [A whole genome amplification protocol for a wide variety of DNAs, including those from formalin-fixed and paraffin-embedded tissues.](#) Score: 59.86
 PL Paris. *Methods in molecular biology* (Clifton, N.J.), 2009, , 556(1): 89-98. PMID: 19488873 Ratio:0.58

11 [Perspectives of DNA methylation in forensic genetics and new promises of its detection methods.](#) Score: 58.86
 SM Zhao, CT Li. *Fa yi xue za zhi*, 2009, Aug., 25(4): 290-5. PMID: 19788082 Ratio:0.57

Relevancy Threshold (Similarity ratio = 0.56). Entries above here have an unusual level of similarity

12 [Methylsugar permeability in representatives within the genome of a *M. m. fumigatus* hybrid correlate with double minute chromosome formation.](#) Score: 58.31
JD Brown, D Golden, RJ O'Neill. *Genomics*, 2008, Mar, , 91(3): 267-73. PMID: 18226492 Ratio:0.56

13 [Evaluation of whole genome amplification using multiple displacement amplification of a limited number of cells.](#) Score: 57.84
S Bashirades, N Salame, PC Patsalis. *Clinical chemistry and laboratory medicine : CCLM / FESCC*, 2006, , 44(9): 1158-60. PMID: 16958614 Ratio:0.56

14 [Evaluation of whole genome amplification protocols for array and other nucleic acid CGH.](#) Score: 57.72
A Hittelman, S Sridharan, R Roy, J Priddyam, M Loda, C Collins, PL Paris. *Diagnostic molecular pathology : the American journal of surgery*, 2007, Dec, , 164(4): 198-206. PMID: 18043282 Ratio:0.55

15 [Whole genome amplification of the rat *Peromyscus gossypinus* L. as a tool from single cells.](#) Score: 56.54
Y Wang, M Zhu, R Zhang, H Yang, Y Wang, G Sun, S Jin, T Hsiao. *Journal of microbiological methods*, 2009, May, , 77(2): 229-34. PMID: 19233233 Ratio:0.54

16 [A whole genome amplification method to generate long fragments from low quantities of genomic DNA.](#) Score: 56.34
R Kitterl, M Stoneking, M Kayser. *Analytical biochemistry*, 2002, Jan, , 300(2): 237-44. PMID: 11779116 Ratio:0.54

17 [Whole genome amplification of sodium borohydride treated DNA shows the accurate numbers of methylized cytosine density in treated DNA samples.](#) Score: 55.81
J Mill, S Yazdanpanah, E Guckel, S Ziegler, Z Kaminsky, A Petronis. *BioTechniques*, 2006, Nov, , 41(5): 603-7. PMID: 17140118 Ratio:0.54

18 [Determining the global DNA methylation status of rat according to the identifier repetitive elements.](#) Score: 55.81
HH Kim, JH Park, KS Jeong, S Lee. *Electrophoresis*, 2007, Nov, , 28(21): 3854-61. PMID: 17960839 Ratio:0.54

19 [Coupling DNA methylation from small amounts of genomic DNA starting material: efficient random bisulfite conversion and subsequent whole genome analysis.](#) Score: 55.61
J Mill, A Petronis. *Methods in molecular biology* (Clifton, N.J.), 2009, , , 507(1): 371-81. PMID: 18987828 Ratio:0.53

20 [Analysis of DNA methylation by amplification of un methylated sites \(AIMS\).](#) Score: 54.05
M Jordà, J Rodriguez, J Frigola, MA Peinado. *Methods in molecular biology* (Clifton, N.J.), 2009, , , 507(1): 107-16. PMID: 18987810 Ratio:0.52

21 [Genome-wide divergence of DNA methylation marks in cerebral and cerebellar cortices.](#) Score: 53.68
Y Xin, B Charnier, MM Liu, H Galfavy, R Costa, B Ilievska, G Rosokljak, V Arango, AJ Dwork, JI Mann, B Tycko, F Highfill. *PloS one*, 2010, , 5(6): e11357. PMID: 20596539 Ratio:0.52

22 [SNP-based chromosomal copy number reconstitution following multiple displacement whole genome amplification.](#) Score: 53.67
JJ Cornveaux, MC Krue, D Hu-Lince, KE Ramsey, VL Zismann, DA Stephan, DW Craig, MJ Huettelman. *BioTechniques*, 2007, Jan, , 42(1): 77-83. PMID: 17269488 Ratio:0.52

23 [A genome-wide analysis of brain DNA methylation identifies new candidate genes for geographic language lateral sclerosis.](#) Score: 53.39
JM Morahan, B Yu, RJ Trent, R Pamphlett. *Amyotrophic lateral sclerosis : official publication of the Wor*, , , 10(5-6): 418-29. PMID: 19922134 Ratio:0.51

24 [Epigenetic profiling of the H19 differentially methylated region and comprehensive whole genome array-based analysis in Silver-Russell syndrome.](#) Score: 53.36
SY Lin, CN Lee, CC Hung, WY Tsai, SP Lin, NC Li, WS Hsieh, YC Tung, DM Niu, WM Hsu, LY Chen, MY Fang, MP Tu, PW Kuo, CY Lin, YN Su, HN Ho. *American journal of medical genetics. Part A*, 2010, Oct, , 152(A10): 2521-8. PMID: 20830799 Ratio:0.51

25 [The use of multiple displacement amplified DNA as a control for methylation specific PCR, pyrosequencing, bisulfite sequencing and methylation sensitive restriction enzymes PCR.](#) Score: 52.66
S Hughes, JL Jones. *BMC molecular biology*, 2007, , 8(1): 91. PMID: 17939862 Ratio:0.51

26 [Measuring the genome landscape using tiling array technology.](#) Score: 51.34
J Yazaki, BD Gregory, JR Ecker. *Current opinion in plant biology*, 2007, Oct, , 10(5): 534-42. PMID: 17703988 Ratio:0.49

27 [Synthesis of universal unmethylated control DNA by nested whole genome amplification with phi29 DNA polymerase.](#) Score: 51.27
N Umetani, MF de Maat, T Mori, H Takeuchi, DS Hoon. *Biochemical and biophysical research communications*, 2005, Apr, , 329(1): 219-23. PMID: 15721296 Ratio:0.49

28 [Genefinder software to de-novo genes estimation for whole genome sequencing by long-range PCR analysis.](#) Score: 49.63
N Ben Zikra, M Gautier, R Andonov, D Laverm, MF Cochet, P Vobe, A Sorokin, Y Le Loir. *Nucleic acids research*, 2004, , , 32(1): 17-24. PMID: 14704339 Ratio:0.48

29 [Mutations of TSH3 induce loss of DNA methylation and amplification of the TSHZ3 gene.](#) Score: 49.41
AF Nasr, M Nutini, B Palombo, E Guerra, S Alberti. *Oncogene*, 2003, Mar, , 22(11): 1668-77. PMID: 12642870 Ratio:0.48

30 [The epigenetic lifestyle and LNA methylation](#) Score: 49.1
J Geisel, H Schorr, M Bodis, S Iaber, U Hubner, JP Knapp, R Obed, W Hermann. Clinical chemistry and laboratory medicine : CCLM / FESCC, 2005, , 43(10): 1164-9. PMID: 16197315 Ratio:0.47

31 [Two methods of whole-genome amplification enable accurate genome-wide SNP linkage analysis across a 5320 SNP linkage map](#) Score: 48.47
DL Barker, MS Hansen, AF Faruqi, D Giannola, OR Insula, RS Lasken, M Lutterich, V Makarov, A Olliphant, JH Pinter, R Shen, I Slepisova, W Ziebler, E Lai. Genome research, 2004, May, , 14(5): 901-7. PMID: 15153887 Ratio:0.47

32 [Development of the first ddNA sequencing of *Ornithodoros* mite genome using multiple displacement amplification of rare-copy sequences of 11000 dinucleotides](#) Score: 47.45
Y Wang, RG Kleespies, MB Ramle, JA Jehle. Journal of virological methods, 2008, Sep, , 152(1-2): 106-8. PMID: 18598718 Ratio:0.46

33 [Whole genome amplification with Pfu29 DNA polymerase to enable genome-wide genomic analysis of samples of low DNA yield](#) Score: 46.96
K Silander, J Saarela. Methods in molecular biology (Clifton, NJ), 2008, , 439(1): 1-18. PMID: 18370092 Ratio:0.45

34 [Whole genome amplification on only \(unaffiliated\) microtubule](#) Score: 45.11
L Chen, A Manz, PJ Day. Analytical biochemistry, 2008, Jan, , 372(1): 128-30. PMID: 17949674 Ratio:0.43

35 [Application of DNA tiling arrays for whole-genome analysis](#) Score: 44.51
TC Mockler, S Chan, A Sundaresan, H Chen, SE Jacobsen, JR Ecker. Genomics, 2005, Jan, , 85(1): 1-15. PMID: 15607417 Ratio:0.43

36 [Whole genome multiple displacement amplification from single cells](#) Score: 44.09
C Spits, C Le Caigne, M De Rycke, L Van Haute, A Van Steirteghem, I Liebaers, K Sermon. Nature protocols, 2006, , 1(4): 1965-70. PMID: 17487184 Ratio:0.42

37 [Retention of marker genome sequencing](#) Score: 43.53
JF Costello, DJ Smitaglia, C Plass. Methods (San Diego, Calif.), 2002, Jun, , 27(2): 144-9. PMID: 12095273 Ratio:0.42

38 [How molecular genetics for the prevention of tumor and cancer-prone diseases: anomalous DNA methylation](#) Score: 42.47
G De Palma, P Mozzoni. Giornale italiano di medicina del lavoro ed ergonomia, , , 31(1): 51-3. PMID: 19558040 Ratio:0.41

39 [Genome-wide association of bit-long H1 histone methylation with CHG DNA methylation in Arabidopsis thaliana](#) Score: 42.36
YV Bermatavichute, X Zhang, S Cokus, M Pellegrini, SE Jacobsen. PloS one, 2008, , 3(9): e3156. PMID: 18776934 Ratio:0.41

40 [What's genome amplification and its use as embryo of single bacterial cells](#) Score: 41.22
S Rodriguez, RR Malmstrom, AM Berlin, BW Birren, MR Henn, SW Chisholm. PloS one, 2009, , 4(9): e6864. PMID: 19724646 Ratio:0.4

41 [Highly efficient PCR strategy to discriminate atypical DNA methylation status using whole genome amplification](#) Score: 41.18
Y Yamada, T Ito. BMC research notes, 2011, , 4(4): 179. PMID: 21663670 Ratio:0.4

42 [Evaluation of 3 methods of whole genome amplification for subsequent methylation comparative genomic hybridization](#) Score: 41.17
G Ng, I Robertis, N Coleman. Diagnostic molecular pathology : the American journal of surgery, 2005, Dec, , 14(4): 203-12. PMID: 16319690 Ratio:0.4

43 [Detection and analysis of mitochondrial DNA deletions by whole genome PCR](#) Score: 39.35
CH Tengen, CT Moraes. Biochemical and molecular medicine, 1996, Jun, , 58(1): 130-4. PMID: 8809354 Ratio:0.38

44 [More DNA: sequencing strategies and genome resequencing](#) Score: 39.2
RJ Okagaki, RL Phillips. Genome biology, 2004, , 5(5): 223. PMID: 15128439 Ratio:0.38

45 [Study of tissue-specific CpG methylation of DNA in mouse brain and testes](#) Score: 39.1
TL Azhikina, ED Sverdlov. Biochemistry. Biokhimiia, 2005, May, , 70(5): 596-603. PMID: 15948713 Ratio:0.38

46 [Whole genome amplification from a single cell: implications for genetic analysis](#) Score: 39
L Zhang, X Cui, K Schmidt, R Hubert, W Navidi, N Arnhelm. Proceedings of the National Academy of Sciences of the United States of America, 1992, Jul, , 89(13): 5847-51. PMID: 1631067 Ratio:0.37

47 [Whole genome amplification: abundant quantities of DNA from precious samples for clinical applications](#) Score: 37.59
RS Lasken, M Egholm. Trends in biotechnology, 2003, Dec, , 21(12): 531-5. PMID: 14624861 Ratio:0.36

48 [Fidelity of whole genome amplification of blood spot DNA for RFLP typing and SNP analysis](#) Score: 37.59
KK Singh, SA Spector. Clinical genetics, 2007, Aug, , 72(2): 156-9. PMID: 17661821 Ratio:0.36

49 [Whole genome amplification of DNA from residual cells left by accidental passage](#) Score: 37.59
Ratio:0.36

KJ Sorensen, K Turielau, G Vrankovich, J Williams, AT Christian. Analytical biochemistry, 2004, Jun, , 324(2): 312-4. PMID: 14690700 Score: 37.59 Ratio:0.36

50 Improved efficiency of whole genome amplification from bacterial cells. YM Kwon, MM Cox. BioTechniques, 2004, Jul, , 37(1): 40, 42, 44. PMID: 15283198 Score: 37.38 Ratio:0.36

51 Genome-wide, lympho-regulatory lDNA methylation profiling using bisulfite-mediated cytosine conversion. J Reinders, C Delucinge Vivier, G Theiler, D Chollet, P Descombes, J Paszkowski. Genome research, 2008, Mar, , 18(3): 469-76. PMID: 18218979 Score: 37.18 Ratio:0.36

52 Whole genome amplification of uterine regulating LNA enabled comprehensive screening for allelic imbalance in uterine. J Li, L Harris, H Mamon, MH Kulke, WH Liu, P Zhu, G Mike Makrigiorgos. The Journal of molecular diagnostics : JMD, 2006, Feb, , 8(1): 22-30. PMID: 16436631 Score: 36.93 Ratio:0.36

53 Amplification of bisulfite-converted DNA for genome-wide LNA methylation profiling. J Reinders. Cold Spring Harbor protocols, 2009, Dec, , 2009(12): pdb.prot5342. PMID: 20150089 Score: 36.46 Ratio:0.35

54 Genome-wide, deep, unbiased archiving of frozen biopsy tissue samples. MV Hollegaard, J Graaholm, A Borgham, M Nygaard, B Norgaard-Pedersen, T Ørntoft, PB Mortensen, C Wiuf, O Mors, M Dideriksen, P Thorsen, DM Hougaard. BMC genomics, 2009, , 10(2): 297. PMID: 19575812 Score: 36.46 Ratio:0.35

55 Whole-genome amplification of oral fluid cell-cultured DNA in a population-based case-control study of breast cancer. X Liang, A Trentham-Dietz, L Titus-Ernstoff, PA Newcomb, RA Welch, AA Hutchinson, JM Hampton, CB Sutcliffe, JL Haines, KM Egan. Cancer epidemiology, biomarkers prevention : a publication of, 2007, Aug, , 16(8): 1610-4. PMID: 17684135 Score: 36.39 Ratio:0.35

56 Virtual genome scan: a tool for rapid and inexpensive analysis of the human genome. JM Rouillard, E Enson, R Kuick, J Asakawa, K Wimmer, M Muleris, EM Petty, S Hanash. Genome research, 2001, Aug, , 11(8): 1453-9. PMID: 11483587 Score: 36.06 Ratio:0.35

57 Multiple primers rolling-circle amplification method for the amplification of circular DNA viruses. H Stevens, A Rector, M Van Ranst. Cold Spring Harbor protocols, 2010, Apr, , 2010(4): pdb.prot5415. PMID: 20360369 Score: 35.74 Ratio:0.34

58 Study on application of the whole genome amplification in LCN. HG Zhou, C Zhang, Fai yue za zhi, 2006, Feb, , 22(1): 43-4, 47. PMID: 16524185 Score: 35.34 Ratio:0.33

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60 Detection of conserved methylation and mapping of a gene influencing cytosine methylation in the genome of *Citrus*. Q Cai, CL Guy, GA Moore. Genome / National Research Council Canada = Génome / Conseil can. 1996, Apr, , 39(2): 235-42. PMID: 8984000 Score: 34.38 Ratio:0.33

61 Singleton birth after nonconsanguineous genetic diagnosis for Huntington disease using whole genome amplification. JF Chow, WS Young, EY Lau, ST Lam, TT Tong, EH Ng, PC Ho. Fertility and sterility, 2009, Aug, , 92(2): 828.e7-10. PMID: 19515365 Score: 34.34 Ratio:0.33

62 Rolling-circle amplification of viral DNA genomes using phi29 polymerase. R Jolne, H Müller, A Rector, M van Ranst, H Stevens. Trends in microbiology, 2009, May, , 17(5): 205-11. PMID: 19375325 Score: 34.04 Ratio:0.33

63 Primer design for Whole Genome Amplification using genetic algorithms. AE Png, KW Cho, CI Lee, SH Leong, OL Kon. In silico biology, 2006, , 6(6): 505-14. PMID: 17518761 Score: 33.69 Ratio:0.32

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65 DNA methylation and the functional organization of the nuclear compartment. J Espada, M Esteller. Seminars in cell developmental biology, 2010, Apr, , 21(2): 238-46. PMID: 19892028 Score: 31.57 Ratio:0.3

66 Whole genome amplification and genetic analysis after extraction of nucleic acid from dried blood spots. MV Hollegaard, KM Sorensen, HK Petersen, MB Armandotier, B Norgaard-Pedersen, P Thorsen, DM Hougaard. Clinical chemistry, 2007, Jun, , 53(6): 1161-2. PMID: 17517589 Score: 30.07 Ratio:0.29

67 Self-priming arms for modified random oligonucleotides: facilitating the quality control of whole genome amplification. I Brakner, B Paquin, M Belouchi, D Labuda, M Krajinicovic. Analytical biochemistry, 2005, Apr, , 339(2): 345-7. PMID: 15797576 Score: 30.07 Ratio:0.29

68 Comparing whole genome amplification methods and sources of biological samples for single nucleotide polymorphism genotyping. Score: 30.07 Ratio:0.29

JW Park, TH Beaty, P Boyce, AF Scott, I McIntosh. Clinical chemistry, 2005, Aug., 51(8): 1520-3. PMID: 16040848 Score: 29.85 Ratio:0.29

69 [\[16\(2-ethylhexyl\)phosphate increases the DNA methylation level of genes in the mouse brain\]](#) SD Wu, J Zhu, YS Li, LQ Gan, XG Yuan, MD Xu, GH Wei. Zhonghua nan ke xue = National journal of andrology, 2009, Oct., 15(10): 876-81. PMID: 20112733 Score: 29.65 Ratio:0.29

70 [Comparing human genomic amplification using multiple displacement amplification](#) FB Dean, S Hosono, I Fang, X Wu, AF Faruqi, P Bray-Ward, Z Sun, Q Zong, Y Du, J Du, M Driscoll, W Song, SF Kingsmore, M Egholm, RS Lasken. Proceedings of the National Academy of Sciences of the United States of America, 2002, Apr., 99(8): 5261-6. PMID: 11959976 Score: 29.65 Ratio:0.29

71 [Variation pattern of total tRNA and rRNA methylation in animals](#) AP Bird, MH Taggart. Nucleic acids research, 1980, Apr., 8(7): 1485-97. PMID: 6253987 Score: 28.4 Ratio:0.27

72 [Multiple displacement amplification of the entire genome from single cells](#) KV Schwabert, J Fredrickson, AR Thorholt. Methods in molecular medicine, 2007, , 132(2): 87-99. PMID: 17876078 Score: 27.8 Ratio:0.27

73 [Whole genome amplification of single cells: mathematical analysis of FEP and tagged PCR](#) F Sun, N Arbehn, MS Waterman. Nucleic acids research, 1995, Aug., 23(15): 3034-40. PMID: 7659528 Score: 27.19 Ratio:0.26

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75 [A whole genome mouse BAC microarray with 1-Mb resolution for analysis of DNA copy number changes by array comparative genomic hybridization](#) YJ Chung, J Jonkers, H Kitson, H Fiegler, S Humphrey, C Scott, S Hunt, Y Yu, I Nishijima, A Velds, H Holstege, N Carter, A Bradley. Genome research, 2004, Jun., 14(1): 188-96. PMID: 14707179 Score: 25.05 Ratio:0.24

76 [Whole genome cloning using linear microdissection tissue](#) CM Feltmate, SC Mok. Methods in molecular biology (Clifton, N.J.), 2005, , 293(1): 69-77. PMID: 16028411 Score: 24.65 Ratio:0.24

77 [ReMAP: whole genome healing reference MAPping program](#) Y Xi, W Li. BMC bioinformatics, 2009, , 10(1): 232. PMID: 19635165 Score: 23.99 Ratio:0.23

78 [The combination of high efficient cloning of the whole genome sequence of hepatitis B virus](#) BY Xu, YM Wang, L Lang, YP Huang. Zhonghua gan zang bing za zhi = Zhonghua ganzangbing zazhi = Ch, 2005, Sep., 13(9): 704-6. PMID: 16174469 Score: 23.48 Ratio:0.23

79 [Population of genome-wide DNA fragment libraries using bisulfite in polyacrylamide gel electrophoresis, sites, with formation denaturation and single strand for matured circular restriction by oligonucleotide ligation and detection](#) SS Ranade, CB Chung, G Zou, VL Boyd. Analytical biochemistry, 2009, Jul., 390(2): 126-35. PMID: 19379703 Score: 23.22 Ratio:0.22

80 [Analysis and accurate quantification of Cyt/5 methylation by MALDI mass spectrometry](#) J Tost, P Schatz, M Schuster, K Berlin, JG Gut. Nucleic acids research, 2003, May., 31(9): e50. PMID: 12711695 Score: 21.96 Ratio:0.21

81 [Preliminary genetic diagnosis of Marfan syndrome using multiple displacement amplification](#) B Lledó, J Ten, FM Galán, R Bernabeu. Fertility and sterility, 2006, Oct., 86(4): 949-55. PMID: 17027361 Score: 21.62 Ratio:0.21

82 [Evaluation of whole genome amplification methods using neurofibroma brain samples](#) K Iwamoto, J Ueda, Y Nakano, M Bundo, W Ukai, E Hashimoto, T Saito, T Kato. Journal of neuroscience methods, 2007, Sep., 165(1): 104-10. PMID: 17604841 Score: 21.57 Ratio:0.21

83 [Novel subtelomeric and Ndel specific microarrays to detect copy number and methylation changes in whole genomes](#) J Li, A Protopopov, F Wang, V Schenkova, V Petushkov, O Vorontsova, L Petrenko, V Zaburovska, O Muravenko, E Braga, L Kisselev, MI Lerman, V Kashiuba, G Klein, I Emborg, C Wahlestedt, ER Zaborsky. Proceedings of the National Academy of Sciences of the United States of America, 2002, Aug., 99(16): 10724-9. PMID: 12149436 Score: 21.46 Ratio:0.21

84 [Genomic identity of clones and methods to explore tRNA](#) B de Moner, I Boulanger, S Taouri, JP Renard, A Eggen. Cloning and stem cells, 2004, , 6(2): 133-9. PMID: 15268787 Score: 20.68 Ratio:0.2

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86 [Whole methylation analysis by ultra-deep sequencing using non-base coding](#) CA Bormann Chung, VL Boyd, KJ McKernan, Y Fu, C Monighetti, HE Peckham, M Barker. PLoS one, 2010, , 5(2): e9320. PMID: 20179767 Score: 20.57 Ratio:0.2

87 [Amplifying whole mouse genome with multiple displacement amplification](#) Score: 19.93 Ratio:0.19

N Gorrochotegui-Escalante, WC Black. Insect molecular biology, 2003, Apr, , 12(2): 195-200. PMID: 12653941

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90 [Comparative molecular analysis of whole genome.](#) S Cheng, R Higuchi, M Stoneking. Nature genetics, 1994, Jul, , 7(3): 350-1. PMID: 7920652

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